

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Griffith, Irwin J.
Pollock, Joanne
- (ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen
- (iii) NUMBER OF SEQUENCES: 25
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
 - (B) STREET: 46th Floor - 1 Liberty Place
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hohenschutz, Liza D.
 - (B) REGISTRATION NUMBER: 33,712
 - (C) REFERENCE/DOCKET NUMBER: IMPH-0001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (215) 568-3100
 - (B) TELEFAX: (215) 568-3439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1337 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Crytpomeria japonica
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 66..1187

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 129..1187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC      60
AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT      107
Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe
-21 -20 -15 -10

GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA      155
Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg
-5 1 5

GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA      203
Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala
10 15 20 25

GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT      251
Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr
30 35 40

ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT      299
Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr
45 50 55

CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT      347
Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser
60 65 70

GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT      395
Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr
75 80 85

AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT      443
Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly
90 95 100 105

CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG      491
Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu
110 115 120

TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC      539
Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn
125 130 135

GAG AGT TTT GGG GTG GAG CCT GTT CAT CCT CAG GAT GGC GAT GCT CTT      587
Glu Ser Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu
140 145 150

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[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe Val Ile
-21 -20                               -15                -10

Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp
-5      1      5      10

Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val Gly
      15      20      25

Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr Thr Val
      30      35      40

Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr Leu Arg
      45      50      55

Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn
      60      65      70      75

Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr
      80      85      90

Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys
      95      100      105

Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu Tyr Leu
      110      115      120

Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn Glu Ser
      125      130      135

Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu
      140      145      150      155

Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser
      160      165      170

Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr Ile
      175      180      185

Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His
-190- -195                -200-

Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe

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205					210					215					
Asn 220	Gln	Phe	Gly	Pro	Asn 225	Cys	Gly	Gln	Arg	Met 230	Pro	Arg	Ala	Arg	Tyr 235
Gly	Leu	Val	His	Val 240	Ala	Asn	Asn	Asn	Tyr 245	Asp	Pro	Trp	Thr	Ile 250	Tyr
Ala	Ile	Gly	Gly 255	Ser	Ser	Asn	Pro	Thr 260	Ile	Leu	Ser	Glu	Gly 265	Asn	Ser
Phe	Thr	Ala 270	Pro	Asn	Glu	Ser	Tyr 275	Lys	Lys	Gln	Val	Thr 280	Ile	Arg	Ile
Gly	Cys 285	Lys	Thr	Ser	Ser	Ser 290	Cys	Ser	Asn	Trp	Val 295	Trp	Gln	Ser	Thr
Gln 300	Asp	Val	Phe	Tyr	Asn 305	Gly	Ala	Tyr	Phe	Val 310	Ser	Ser	Gly	Lys	Tyr 315
Glu	Gly	Gly	Asn	Ile 320	Tyr	Thr	Lys	Lys	Glu 325	Ala	Phe	Asn	Val	Glu 330	Asn
Gly	Asn	Ala	Thr 335	Pro	Gln	Leu	Thr	Lys 340	Asn	Ala	Gly	Val	Leu 345	Thr	Cys
Ser	Leu	Ser	Lys	Arg	Cys										

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAYAAAYCCNA THGAYWS

17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGAATTCAA YTGGGCNCAR AAYSG

25

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTGCAGCCRT TYTCNACRTT RAA

23

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCATNCKRT TYTGNGCCCA

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGCAGCKR TTYTGNGCCC AARTT

25

(2) INFORMATION FOR SEQ ID NO:8:-

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGATTCCC CTTGCTTA

18

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAATTCGA TAATCCCATA GACAGC

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCCTATGT ACATTGC

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAATGTACA TAGGCAT

17

(2) INFORMATION FOR SEQ ID-NO:12: - - - - -

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCAATTCTT CTGATGGT

18

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTGTCAAT TGAGGAGT

18

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTGCAGAAG CTTCAATCAAC AACGTTTAGA

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAGAACTCCA GTCGAAGT

18

--(2) INFORMATION FOR SEQ ID NO:16:--

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAGCTCTCAT TTGGTGC

17

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TATGCAATTG GTGGGAGT

18

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Cryptomeria japonica*
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /note= "the amino acid at position 7 is Ser, Cys, Thr, or His"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp	Asn	Pro	Ile	Asp	Ser	Xaa	Trp	Arg	Gly	Asp	Ser	Asn	Trp	Ala	Gln
1				5					10					15	
Asn Arg Met Lys															
20															

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Cryptomeria japonica*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu	Ala	Phe	Asn	Val	Glu	Asn	Gly	Asn	Ala	Thr	Pro	Gln	Leu	Thr	Lys
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGGTCTAGAG GTACCGTCCG ATCGATCATT

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGTCTAGAG GTACCGTCCG

20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATGATCGAT GCT

13

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGAATTCTCT AGACTGCAGG T

21

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTT

35

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Juniperus sabinoides

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Asn Pro Ile Asp
1 5